

**Figure 1**

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MshC nucleic acid sequence of *M. smegmatis*

ATGCAATCGTGGTCGGCACCGCGATTCCGGTGGTCCGGGACGTGGCCCTGCGCTG  
CGCCTCTCGACAGCGCTGATGCCAGGTCCGGCCCGTCACACCGGGACCGACCGC  
AACCATGTACGTGTGCGGCATCACCCATACGACGCGACCCATCTGGGTACGCCGC  
GACCTATCTGACGTTGACCTGGTCATGCCATGGCTCGACGCCGGACACACCGT  
GCAGTACGTCCAGAACGTCACCGACGTGGACGACCCGTTGTCAGCGTGCTGAGC  
GCGACGGCATCGACTGGCGGACCGCTGGCGACCGCGAGACGCACTGTTCCGTGAG  
GACATGGCCGCGTTGCGCGTGCTGCCCGCACGACTACGTGCCCGACCGACGC  
GATCGCCGAGGTCGTCGAGATGGTCGAGAACGCTGCTGCCCTGGGTGCGCGTACA  
TCGTCGAGGACGCCGAGTACCCGACGTGTACTTCCGCGCCACGCCACCGCGCAG  
TTCGGGTACGAGTCCGGTACGACCGCGACACCATGCTCACGTTGTCGCCAACGC  
GGCGGGACCCGGACCGCCCGGGCAAGTCCGATCAACTCGACGCGTTGCTGTGGCG  
CGCCGAGCGTCCGGCAGCCAGCTGCCCTCGCCGTTGCCGGGGCCGGCCCG  
GCTGGCACGTGGAATGTTGGCGATGCCCTGACGCCGATGGCACCGGCGCTCGAC  
ATCCAGGGCGGCCAGCGACCTCATCTTCCCGACACGAGTATTGGCCGCGCA  
CGCCGAATCCGTACCGGTGAGCGACGATTGACGCCACTACGTGCACACCGGCA  
TGATCGGCTGGACGCCACAAGATGAGCAAGAGCCGGCAACCTGGCCTGGT  
TCGCAGTTGCGCGCCAGGGCGTCGACCCGTCGGCGATCCGGCTGCCCTGTTCTCC  
GGGCACTACCGCGAGGACCGGTTCTGGAGCAACGAGGTTCTGACGAGGCCAACGC  
GCGACTCGCGCGGTGGCGCAGTGCCACCGCATTGCCGAGGCCCGATGCCGACCG  
ACGTGATCGCGCGCGTCCGGCAGTACCTGGCGATGACCTGGACACGCCGAAAGCG  
CTTGCCGCACTCGATGGTTGGTGTACCGACGCCGCTGTCCTACGGTGGCACGACACC  
GAGTCGCCGCGGCTCGTGGCCACCAACCGTCGACGCCGTTGCTGGGTGTCGACCTC

Figure 2A

MshC amino acid sequence of *M. smegmatis* (PMshCMs)

MQSWSAPAIP VVPGRGPALR LFDSADRQVR PVTPGPTATM  
YVCGITPYDA THLGHAATYL TFDLVHRLWL DAGHTVQYVQ  
NVTDVDDPLF ERAERDGIDW RTLGDRETQL FREDMAALRV  
LPPHDYVAAT DAIAEVVEMV EKLLASGAAY IVEDAEYPDV  
YFRADATAAQF GYESGYDRDT MLTLFAERGG DPDRPGKSDQ  
LDALLWRAER PGEPSWPSPF GRGRPGWHVE CSAIALTRIG TGLDIQGGGS  
DLIFPHHEYS AAHAESVTGE RRFARHYVHT GMIGWDGHKM  
SKSRGNLVLV SQLRAQGVDP SAIRLGLFSG HYREDRFWSN  
EVLDEANARL ARWRSATALP EAPDATDVIA RVRQYLADDL  
DTPKALAALD GWCTDALSYG GHDTESPRLV ATTVDALLGV DL (SEQ ID  
NO: 2)

**Figure 2B**

>cysS2: 1242 bp - *M. tuberculosis* -

atgcagtcgttgtattgcccaccgggtccggtgtgcgggacgaggcccgcagctacgg  
ctgtacgacagcgccgaccggcaggtccgtccgggtggcgcccgatctaaggccaccatg  
tacgtctcgggatcacgcctacgacgccacgcacatctggccatgtgcacccatgt  
acgttcgacactatccatcggtgtggatctcggtcatgaattgcactatgtccag  
aacatcaccgacatcgacgatccactattgagcgcgcggatgcgcacgggtgtcactgg  
cgtgaccttgcuaagccgaggctggccctgtgtgaggacatggcggcgtgcgggtg  
ctaccaccgcaagactacgtggggccaccgaagcgattgctgaaatggcgagctcatc  
gaaaaaatgctggcgtgcggggcggctatgtcatagaccggaaatggagagtaccag  
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catgcggatgatcggtggacggcacaagatgtcaaagagccgcggcaacctcg  
ctgggtcggcgcgtgcgtgcgcaggacgttgagccatcgccgggtcgctgggttgctc  
gccggacactaccgagccgatcggtctggagccagcaggcttgacgaggcgaccgc  
cggctgcaccgttggcgccaccgcacccgcactccgcgggtccggccgcagttgacg  
gtcgctcggtgcgcgcgtaccctggccgacgatctcgatcgccaaagcgattgc  
ctggatgggtgggtcaccgatgcgggtggagttacggcggccacgatgcggggcgcc  
ttgggtggcgacggcgatcgatgcctgctcggtggacctg

Figure 2C

MshC amino acid sequence of *M. tuberculosis* (PMshCMtP1101)

MQSWYCPPVPVLPGPQLRLYDSADRQVRPVAPGSKATMYVCGITPYD  
ATHLGHAATYVTFDLIHRLWLDLGHELHYVQNITDIDDPLFERADRDGVD  
WRDLAQAEVALFCEDMAALRVLPPQDYVGATEAIAEMVELIEKMLACGA  
AYVIDREMGEYQDIYFRADATLQFGYESGYDRDTMLRLCEERGGDPRRPG  
KSDELDALLWRAARPGEPSWPSPFGPGRPGWHVECAAIALSRIGSGLDIQG  
GGSDLIFPHHEFTAHAECVSGERRFARHYVHAGMIGWDGHKMSKSRGN  
LVLVSALRAQDVEPSAVRLGLLAGHYRADRFWSQQVLDEATARLHRWRT  
ATALPAGPAAVDVVARVRRYLADDLDTPKAIAALDGWVTDAVEYGGHD  
AGAPKLVATAIDALLGVDL (SEQ ID NO: 4)

**Figure 2D**

MshC amino acid sequence of *Corynebacterium striatum* (AAG03366) (PMshC-Cor.s-GB)

MHAWPDPSPVPAVAGTPVPLKLFDTADQRVKEVDTPDANGEVGMYVCGITPYDSTHLGHAATYLTFDLAQRQLLANGHKVHYVQNI TDVDDPLFERAERDGVDWRELGTSQINLFRSDMEILSVIPPCDYIGAMESVDEVIAMVQQLDA  
GAAYELDQGDIYASIDATEQFGYESNLDRATMEEYFAERGGDPDREGKRDPLDALVWRGHREGEPAWDSPFGPGRPGWHVECSAIATNRLGSHFAIQGGGSDLAFPHHEFSAAHAEAALKVERMAGHYVHAGMIALDGVKMSKSLGNLVFVHKLSEAGHDPSAIRLAVFAGHYREDRDFS DAILAEAEERLTRWREQLAGEVSEAEATEVVVDKLRAILADDLNTPEALSLLDGAAGDCNQIIATALDGL  
LGVRI (SEQ ID NO: 5)

**Figure 2E**

MshC amino acid sequence of *Streptomyces coelicolor* A3(2) (CAC36366) (PMshCScGB1101)

MHAWPASEVPALPGQGRDLRIHDTATGGPVTLDPGPVARIYVCGITPYD  
ATHMGHAATYNADLVQRVWLDTKRQVHYVQNVTDVDDPLLERAVR  
DGVDWTALAEQETALFREDMTALRMLPPQHYIGAVEAIPGIVPLVERLR  
DAGAAYELEGDVYFSVEADPHFGGVSHLDAATMRLLSAERGGDPDRP  
GKKNPLDPMLWMAAREGEPSWDGGTLGRGRPGWHIECVIAILDHLGM  
GFDVQGGGSDLAFPHHEMGASHAQALTGEFPMAKAYVHAGMVGLDG  
EKMSKSKGNLVFVSQLRREGVDPAIRLTLLAHHYRSDWEWTDQVLQ  
DALARLDRWRAAVSRPDGPPAEALVEEIREALANDLDSPAALAAVDRW  
AALQQESGGTDIGAPGVVSRAVDALLGVAL (SEQ ID NO: 6)

**Figure 2F**

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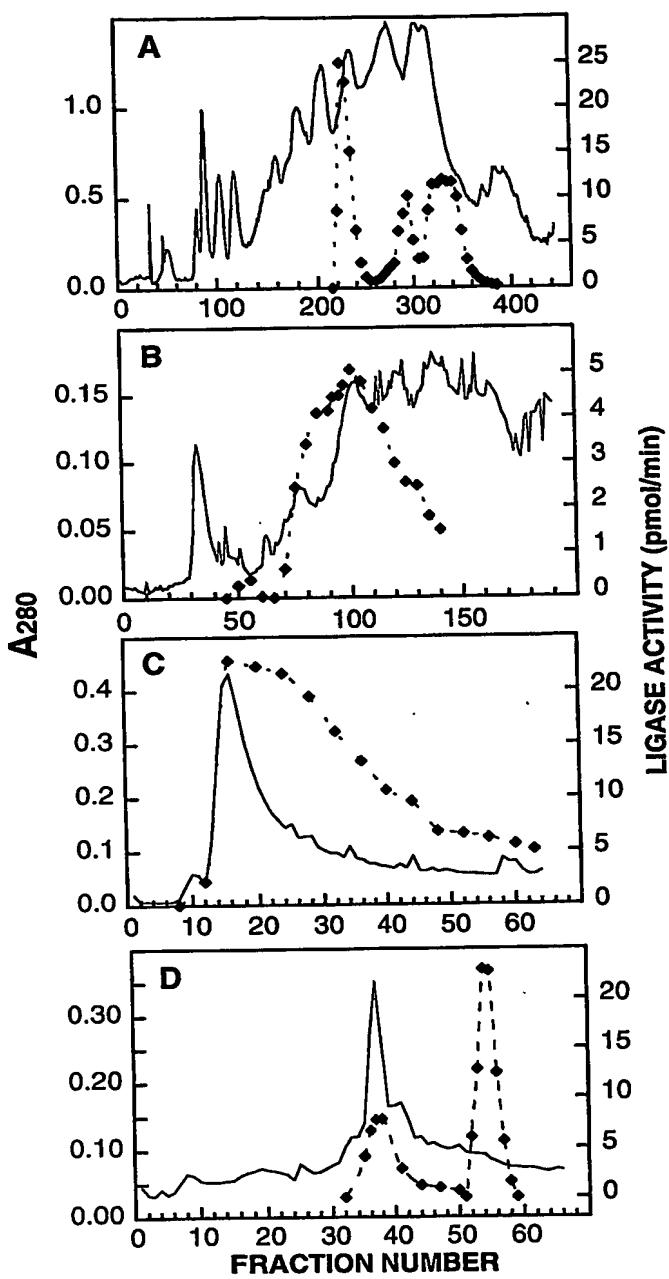


Figure 3

|                                 | 1   | 10   | 20  | 30  | 40  | 50  | 61  |
|---------------------------------|---|--|-----|-----|-----|-----|-----|
| 1. <i>M. smegmatis</i>          | (1)   | <u>YQSWI</u> SAF <small>AI</small> FVMPGRCEA <small>IL</small> RLEDSADROVRPV <small>TP</small> CE <small>IA</small> T--- |     |     |     |     |     |
| 2. <i>M. tuberculosis</i>       | (1)   | <u>YOSWY</u> CEEV <small>VP</small> VL <small>DP</small> GRCEOLRLDSADROVRPV <small>PC</small> SKAT---                    |     |     |     |     |     |
| 3. <i>C. striatum</i>           | (1)   | <u>MHAM</u> EDPSVFAVAGTPVPLKLED <small>IA</small> DRVKEDVLDEDANGEVG <small>MIX</small> CGITPYS---                        |     |     |     |     |     |
| 4. <i>S. coelicolor</i>         | (1)   | <u>MHAM</u> FASEFVALPQGRDLR <small>TH</small> DTGGPVTLDPGP <small>VAR</small> ---  |     |     |     |     |     |
|                                 | 62  | 70   | 80  | 90  | 100 | 110 | 122 |
| 1. <i>M. smegmatis</i> (58)     | <u>TYLTEDL</u> VERLWL <small>PA</small> GH <small>IV</small> OYVONWTDDVDP <small>LF</small> ERAERDGG <small>TD</small> W <small>AR</small> L <small>IG</small> DR <small>ET</small> OLF <small>ER</small> EDMAAL---                   |  |     |     |     |     |     |
| 2. <i>M. tuberculosis</i> (58)  | <u>TYVIEDL</u> TERLWL <small>DI</small> GH <small>E</small> THYVONHTEDDPL <small>ER</small> AD <small>DR</small> DGVD <small>W</small> ARDLAQAEVALF <small>OC</small> EDMAAL  |  |     |     |     |     |     |
| 3. <i>C. striatum</i> (62)      | <u>TYLTEDL</u> AO <small>Q</small> OLANGKXVHYVONWTDDVDP <small>LF</small> ERAERDGGD <small>W</small> AREL <small>GT</small> TSOINL <small>ER</small> SDM <small>ET</small> IL---  |  |     |     |     |     |     |
| 4. <i>S. coelicolor</i> (58)    | <u>TYNA</u> EDLIVORW <small>ML</small> LETRKOVHYVONWTDDVDP <small>LF</small> ERAERDGGD <small>W</small> MTA <small>LE</small> EQETALF <small>ER</small> EDMAAL---   |  |     |     |     |     |     |
|                                 | 123   | 130  | 140 | 150 | 160 | 170 | 183 |
| 1. <i>M. smegmatis</i> (119)    | <u>RVLP</u> PEEDVY <small>AA</small> AT <small>DA</small> IAEV <small>EN</small> VEKLIASGAAIV <small>IV</small> - <u>EDAE</u> Y <small>ED</small> IVYF <small>RA</small> ADAT <small>Q</small> FGYESC <small>YD</small> ---           |  |     |     |     |     |     |
| 2. <i>M. tuberculosis</i> (119) | <u>RVLP</u> PEODVY <small>GA</small> TEAIAEW <small>EL</small> IEKALAGAAIV <small>IV</small> - <u>EDAE</u> Y <small>ED</small> IVYF <small>RA</small> ADAT <small>Q</small> FGYESC <small>YD</small> ---                              |  |     |     |     |     |     |
| 3. <i>C. striatum</i> (123)     | <u>SV</u> TP <small>ED</small> YI <small>GA</small> MESYDEVAW <small>W</small> OOL  |  |     |     |     |     |     |
| 4. <i>S. coelicolor</i> (119)   | <u>RVLP</u> PECHYIGA <small>VE</small> APIG <small>IV</small> PL <small>IV</small> PL <small>IV</small> ERRDGAAAY <small>EG</small> - <u>ED</u> Y <small>EV</small> ADP <small>F</small> EGGV <small>SH</small> IL---                 |  |     |     |     |     |     |
|                                 | 184   | 190  | 200 | 210 | 220 | 230 | 244 |
| 1. <i>M. smegmatis</i> (178)    | <u>EDT</u> WITL <small>FEA</small> ERGGDP <small>DR</small> ECKS <small>SD</small> OLDALLMRAER <small>RP</small> GEPSW <small>PS</small> - <u>FFGR</u> RP <small>GM</small> H <small>VE</small> CSA <small>AI</small> AT---           |  |     |     |     |     |     |
| 2. <i>M. tuberculosis</i> (180) | <u>RTD</u> WIRL <small>CE</small> ERGGD <small>FR</small> EREGKS <small>SD</small> OLDALLMRAAR <small>RP</small> GEPSW <small>PS</small> - <u>FFGP</u> GR <small>PG</small> W <small>HM</small> VECSA <small>AI</small> AT---         |  |     |     |     |     |     |
| 3. <i>C. striatum</i> (179)     | <u>RA</u> TM <small>EY</small> FAERGGDP <small>DR</small> ERGRKL <small>PL</small> DALW <small>GR</small> CHREGEPSW <small>PS</small> - <u>FFGP</u> GR <small>PG</small> W <small>HM</small> VECSA <small>AT</small> ---              |  |     |     |     |     |     |
| 4. <i>S. coelicolor</i> (174)   | <u>AA</u> MRL <small>LSA</small> ERGGDP <small>DR</small> ERGEKKNP <small>LP</small> PMW <small>MA</small> AREGEPSW <small>PS</small> MDGGT <small>LG</small> RCR <small>PG</small> W <small>HM</small> TEC <small>VA</small> TAID--- |  |     |     |     |     |     |
|                                 | 245   | 250  | 260 | 270 | 280 | 290 | 305 |
| 1. <i>M. smegmatis</i> (238)    | <u>RIG</u> GLDIOGGGS <small>SD</small> LI <small>IP</small> PHHEYSAHAESVTGER <small>RE</small> ARH <small>YV</small> H <small>IG</small> MCW <small>D</small> G <small>H</small> KMSKSRGNLIV  |  |     |     |     |     |     |
| 2. <i>M. tuberculosis</i> (240) | <u>RIG</u> SLDIOGGGS <small>SD</small> LI <small>IP</small> PHHEYTAHAECVSGER <small>RE</small> ARH <small>YV</small> H <small>AG</small> MCW <small>D</small> G <small>H</small> KMSKSRGNLIV  |  |     |     |     |     |     |
| 3. <i>C. striatum</i> (239)     | <u>RIG</u> SHFAATOGGGSD <small>LA</small> IFPHHEYSAHAEEAAL  |  |     |     |     |     |     |
| 4. <i>S. coelicolor</i> (235)   | <u>RIG</u> MCFIVOGGGSD <small>LA</small> IFPHHEYASHAOA <small>LT</small> GEFPWAKAY <small>YH</small> AGMCW <small>D</small> LG <small>E</small> NGKMSKSRGNLIV   |  |     |     |     |     |     |
|                                 | 306   | 320  | 330 | 340 | 350 | 360 | 366 |
| 1. <i>M. smegmatis</i> (299)    | <u>IVS</u> QI <small>RA</small> QGVPSA <small>IR</small> GL <small>GI</small> FSCHYREDRF <small>W</small> SN <small>E</small> VLDEAN <small>ART</small> ARW <small>S</small> AT <small>AL</small> PEAF-DATIV                          |  |     |     |     |     |     |
| 2. <i>M. tuberculosis</i> (301) | <u>IVS</u> AI <small>RA</small> QDVPSA <small>IR</small> GL <small>GI</small> LACHYRADEW <small>SC</small> QVLD <small>EA</small> TA <small>RL</small> ARW <small>S</small> AT <small>AL</small> PEAF-AAIV                            |  |     |     |     |     |     |
| 3. <i>C. striatum</i> (300)     | <u>FVHK</u> IS <small>E</small> ACHDPSA <small>IR</small> AVFAGH <small>YR</small> EDRDESDAT <small>IA</small> EA <small>ER</small> ILARW <small>S</small> REOLAGEVSEAAEATEV  |  |     |     |     |     |     |
| 4. <i>S. coelicolor</i> (296)   | <u>FV</u> SIQ <small>R</small> REGVDEA <small>IR</small> ILAHYRS <small>DW</small> EWTLQVLD <small>AL</small> ARLDRM <small>R</small> AVS <small>R</small> EDGE-PAAEAL  |  |     |     |     |     |     |
|                                 | 367   | 380  | 390 | 400 | 410 | 420 |     |
| 1. <i>M. smegmatis</i> (359)    | <u>IVR</u> FOYLAADDL <small>TP</small> KALAALIGW <small>OT</small> DALSYGGH <small>TES</small> ERIV   |  |     |     |     |     |     |
| 2. <i>M. tuberculosis</i> (361) | <u>IVZ</u> RVYRLADDL <small>TP</small> KAIAALIGW <small>OT</small> DAVEYGGH <small>DAGA</small> ERIV  |  |     |     |     |     |     |
| 3. <i>C. striatum</i> (361)     | <u>VDK</u> FAIAADDN <small>TE</small> FALSVLGAGDCN-   |  |     |     |     |     |     |
| 4. <i>S. coelicolor</i> (356)   | <u>VIE</u> ETREALANDL <small>SE</small> AALAAVIRMAQOSEGGIDIGAEGW <small>SR</small> AVDALLGVAI   |  |     |     |     |     |     |

Figure 4

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|                    | 10    | 20  | 30  | 40               | 50                     | 66               |
|--------------------|-------|---|---|------------------|------------------------|------------------|
| 1. MshC M. tuberc. | 1     | 10  | 20  | 30               | 40                     | 50               |
| 2. CysS M. tuberc. | (1)   | MOSWY CPPV PVLPGRPQDRT <b>VSADROVR</b> -- | P VAPGSKATI MYVCGITI EYDATI HICHATI YVIED |                  |                        |                  |
| 3. CysS E. coli    | (1)   | --  | --  | --               | --                     |                  |
|                    | 67    | 80  | 90  | 100              | 110                    | 120              |
| 1. MshC M. tuberc. | (64)  | LIERLWID GHE1 HYVONNTID DEPLI FERZ        | DRDGV DWRLLAOA EVALE FCFM                 | TAIRVLEP ODYVGA  |                        |                  |
| 2. CysS M. tuberc. | (54)  | ILRRMILLARGDYVAFIRNVT                     | EDKILAKA                                  | AAAGREWVWAA      | THERAETAA              |                  |
| 3. CysS E. coli    | (49)  | VVARYLRFELGYKL                            | KYVRNNTID                                 | DDDKI IKRANENGES | EVAMVDRMIAEMHKD        | EDAINNIRE DMEPRA |
|                    | 133   | 140                                       | 150                                       | 160              | 170                    | 180              |
| 1. MshC M. tuberc. | (130) | TEAIAEMWELIEKMIACCLAY                     | TEREMGEYOLIY                              | FRADATLOFGYES    | GYERDTMRLICFEERGCD     | PR               |
| 2. CysS M. tuberc. | (120) | IGHITOMWEMTIERLIOA                        | GHAYTG                                    | GGDGVY FDWLSYFEG | GOLLSCHKTTDDVHOGEGVAAC | --               |
| 3. CysS E. coli    | (115) | TEHIAETIEETIEOLIAK                        | GHAYVAE                                   | --               | NGDMWEDVPTDPTGYVLSROD  | DQGARVMDVVD      |
|                    | 199   | 210                                       | 220                                       | 230              | 240                    | 250              |
| 1. MshC M. tuberc. | (196) | RPGKSDDELALLMPAARPGEPSWPSP                | EGPGRPGMW                                 | HVTECAATL        | SRIGSGID               | TOGCCSDLI        |
| 2. CysS M. tuberc. | (177) | --KRDORDFTLWKGEKPGEPSPWP                  | 1P  | MGRGRPGWHL       | PEFD                   | IEPHH            |
| 3. CysS E. coli    | (175) | --KRNPDWDEVLMKNSKEGEPSPW                  | BSPNGA                                    | GRPGWHIEC        | SAMNCKOLGNHD           | IHGGECSDLMEPHHEN |
|                    | 265   | 270                                       | 280                                       | 290              | 300                    | 310              |
| 1. MshC M. tuberc. | (262) | TAAHZ ECVS GERRFARHYVHA                   | GMIEGDGHKMSKSE                            | GENL             | VIVISAIRACDVEP         | SAVRLGIA         |
| 2. CysS M. tuberc. | (240) | ETAOSSRAAGDC                              | PARY                                      | WLNQW            | TMGSEKMSKSLGNV         | ISMEAM           |
| 3. CysS E. coli    | (238) | ETAOSSICAHDCO                             | YVN                                       | YMHSGMMW         | DREKMSKSLGNF           | ETWRDV           |
|                    | 331   | 340                                       | 350                                       | 360              | 370                    | 380              |
| 1. MshC M. tuberc. | (328) | RFWSOQVILDEATAR                           | HRWRTATALP                                | --               | AGPAA VEVVARVRR        | VIADDL           |
| 2. CysS M. tuberc. | (303) | TEFSE                                     | TAWODAVKAVY                               | GLDEI            | HRVTRVCAVCP            | TAI              |
| 3. CysS E. coli    | (302) | TINSE                                     | EN  | TKOARA           | FEA                    | FEA              |
|                    | 397   | 410                                       | 420                                       | 430              | 440                    | 450              |
| 1. MshC M. tuberc. | (390) | E-YGGHDACAPKL                             | WIAIADAT                                  | ICVDI            | --                     |                  |
| 2. CysS M. tuberc. | (369) | RA1DAGHDGAI                               | SASA                                      | IRAMC            | CDP1                   | DORMESRDETSAA    |
| 3. CysS E. coli    | (368) | RA1KAE                                    | AMANA                                     | MASHLIRK         | SGAOADDSEVAE           | TEAL             |
|                    | 463   | 470                                       | 480                                       | 493              | 498                    |                  |
| 2. CysS M. tuberc. | (434) | NWALADEIRGRIKRA                           | AGIEVTE                                   | LADEPOWSSL       | LGDTK                  |                  |
| 3. CysS E. coli    | (431) | DWAADARDRIN                               | EN  | GT               | VLEFCPOET              | TMRK             |

Figure 5

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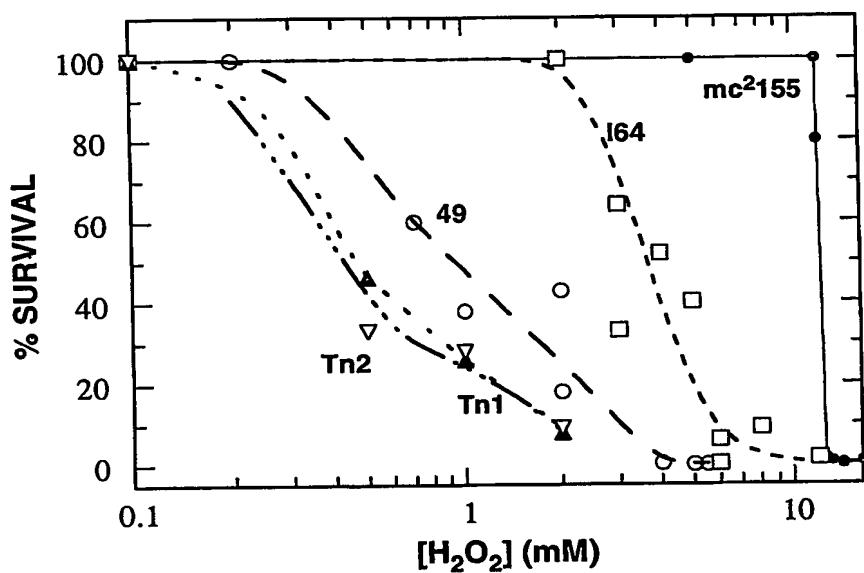


Figure 6

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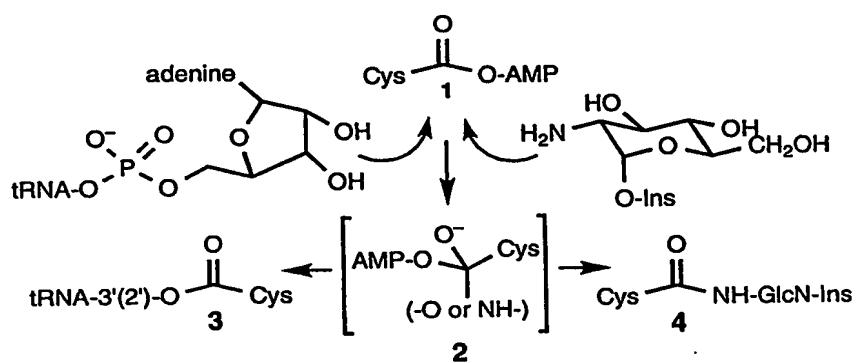


Figure 7

50

|                        |     |  |                 |
|------------------------|-----|--|-----------------|
| <i>M. tuberculosis</i> | (1) | -----VTALDWRSALTADEOORSVRALVTATTAVDGVA | PVGGEQV         |
| <i>M. smegmatis</i>    | (1) | -----VISTEWRTG                         | LTGAQQAEIRALIDA |
| <i>M. leprae</i>       | (1) | -----MVLNWRF                           | ALSADEQRLVREII  |
| <i>S. coelicolor</i>   | (1) | MTSDDTVRPGRPSI                         | ETLAEELTPEQTD   |
| <i>C. diphtheriae</i>  | (1) | -----MIETSLASAS                        | AAALRDRVDEILAA  |

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|                        |      |                   |             |
|------------------------|------|-------------------|-------------|
| <i>M. tuberculosis</i> | (39) | -----LRELGQQRT    | EHLLVAGSRPG |
| <i>M. smegmatis</i>    | (39) | -----LRELGRDRTR   | HLTTDD      |
| <i>M. leprae</i>       | (38) | -----LRELGYDR     | TEHLLVTD    |
| <i>S. coelicolor</i>   | (51) | LOLRGPAREGV       | VHLLLTL     |
| <i>C. diphtheriae</i>  | (39) | -----NGLRR-ADDGHV | HSCVMDS     |

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pfam00583-

|                        |      |                             |                                  |
|------------------------|------|-----------------------------|----------------------------------|
| <i>M. tuberculosis</i> | (87) | RRRGIGTAMARAALAKTAGRNQFWAHG | TLDPARATASALGLVG                 |
| <i>M. smegmatis</i>    | (84) | RRRGIGAAMARIALAECGP         | GARIWAHGNIAAAQAMASSL             |
| <i>M. leprae</i>       | (86) | RRRGVGAAMVRAALAKT           | GGGNRFWAHGTLASARAT               |
| <i>S. coelicolor</i>   | (99) | RGQGHGRALGSA                | LLAASGKRLRIWAHGHSAARHIAQVLGLSL   |
| <i>C. diphtheriae</i>  | (80) | RRQGYGSFLIRHVV              | SQGVKNVAHGDGAGAKAVAKALQLEQTROLLV |

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|                        |       |                |                |
|------------------------|-------|----------------|----------------|
| <i>M. tuberculosis</i> | (137) | RRPL-R--DIP    | PEPTIPD-GVVI   |
| <i>M. smegmatis</i>    | (134) | RRPL-T--DLP-P- | VPDTPGVRI      |
| <i>M. leprae</i>       | (136) | QRSI-R--TIP    | PPMVPDQLGVWV   |
| <i>S. coelicolor</i>   | (149) | RRPL-TGLD      | LPPEPRIPE-GVSV |
| <i>C. diphtheriae</i>  | (128) | AVEGDR         | ILVESAQLOVPS   |

250

|                        |       |             |                          |
|------------------------|-------|-------------|--------------------------|
| <i>M. tuberculosis</i> | (177) | HPEQGGWTAVQ | LAERRGEAWF               |
| <i>M. smegmatis</i>    | (174) | HPEQGGW     | TEHEIDERRNEGWF           |
| <i>M. leprae</i>       | (178) | HPEQGGW     | TQLAERRSEPWF             |
| <i>S. coelicolor</i>   | (191) | HPEQGSIT    | TQRDLDDRKAEPWF           |
| <i>C. diphtheriae</i>  | (176) | HPEQGGW     | DSARLAQARDTQWFRESDVLFLID |

300

|                        |       |               |                  |
|------------------------|-------|---------------|------------------|
| <i>M. tuberculosis</i> | (226) | HED--HPGLGEVY | VLGVDPA          |
| <i>M. smegmatis</i>    | (219) | HD--ASLGEVY   | VLGVDPAQ         |
| <i>M. leprae</i>       | (227) | HAA--HPGLGEVY | VLGDPQAQGRGLG    |
| <i>S. coelicolor</i>   | (234) | HA--EERLGEVY  | VLGIRPD          |
| <i>C. diphtheriae</i>  | (221) | HGLAEGADGEVY  | VVGGLGSAYRRRGLGD |

343

pfam00583-

|                        |       |               |                 |
|------------------------|-------|---------------|-----------------|
| <i>M. tuberculosis</i> | (274) | AVEEPAVILLYVE | SDNVAAVRTY      |
| <i>M. smegmatis</i>    | (260) | --EPTVILLYVE  | ADNSAAVNTYRK    |
| <i>M. leprae</i>       | (270) | SAEPTVMLYVE   | DNVAAARTYERLGF  |
| <i>S. coelicolor</i>   | (273) | --LPTAMLYVD   | ADNKAAVAVYERLG  |
| <i>C. diphtheriae</i>  | (265) | --R--VILYVE   | GDNESARRAYDALGE |

Figure 8

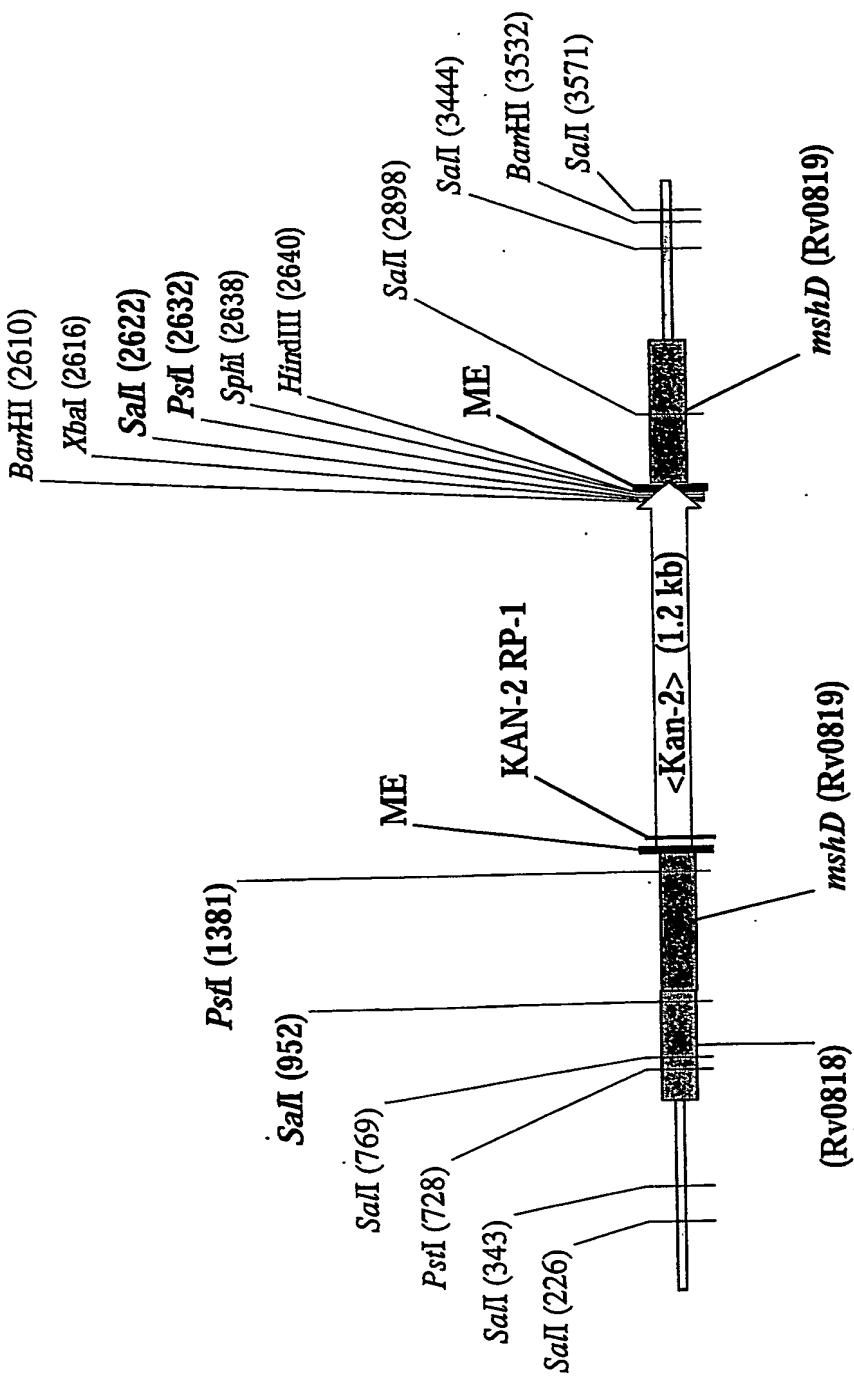


Figure 9

MshD amino acid sequence of *M. tuberculosis* (CAA17625.1) (Rv0819)

MTALDWRSALTADEQRSVRALVTATTAVDGVAPVGEQVLRELGQQRT  
EHLLVAGSRPGPIGYLNLSPPRGAGGAMAELVVHPQSRRRGIGTAMA  
RAALAKTAGRNQFWAHGTLDPARATASALGLVGVRELIQMRRPLRDIP  
EPTIPDGVVIRTYAGTSDDAELLRVNNAAFAGHPEQGGWTAVQLAERR  
GEAWFDPDGLILAFGDSPRERPGRLLGFFHWTKVHPDHPGLGEVYVLGV  
DPAAQRRGLGQMLTSIGIVSLARRLGGRKTLDAVEPAVLLYVESDNVA  
AVRTYQSLGFTTYSVDTAYALAGTDN (SEQ ID NO: 14)

**Figure 10A**

MshD amino acid sequence of *M. smegmatis* (PMshDMs-Tr)

VTSTEWRTGL TGAQQAEIRA LIDAATTHDG VAPVGDQVLR  
ELGRDRTRHL LTTDDDRVVG YLNLAAPAEGD DPAMAEVVH  
PQARRRGIGA AMARTALAEG GPGARIWAHG NIAAAQAMAS  
SLRLVVVREL LQMRRPLTDL PPVPDTPGVR IATYAGPGDD  
AEILRVNNAA FSWHPEQGGW TEHEIDERRN EGWFDPEGLF  
QAFDEQTGSL LGFHWTKIHD ASLGEVYVVG VDPQAQGRGL  
GYTTLIGLH HLAEKLADPE PTVLLYVEAD NSAAVNTYRK  
LGFEVFSVDA AYAAN (SEQ ID NO: 15)

**Figure 10B**

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MshD amino acid sequence of *M. leprae* (ML2193)

MVLNWRFALSADEQRLVREIISAAATEFDEVSPVGEQVLRELGYDRTEHL  
LVTDSRPYAPIIGYLNLSSPRDAGVAMAEVVHPRERRGVGAAMVRA  
ALAKTGGRNRFWAHGTLASARATASVLGLVPVRELVQMQRSLRTIPDP  
MVPDQLGVWVVRTYVGTVDDAELLRVNNAAFAGHPEQGGWTATQLAE  
RRSEPWFDPAGLFLAFGDSSNQPGKLLGFHWTKVHAAHPGLGEVYVL  
GVDPSAQGRGLGQMLTSIGIASLAQRLVGPSAEPVMLYVESDNVAAA  
RTYERLGFTTYSVDTAYALARIDD (SEQ ID NO: 16)

**Figure 10C**

MshD amino acid sequence of *Streptomyces coelicolor* (SCD84.18c, SCO4151)

MTSDDTVRPGRPRSIETLAE LTPEQTDAVLALLTEAARTDGQHAVSEQG  
RLQLRGPA REGVVHLLL TLDGGELVGYAQLEGTD PVEPPAAELVVHPS  
HRGQGHGR ALGSALLAASGKRLRIWAHGGHSAARHLAQVLGLSLFREL  
RQLRRPLTG LDLP E PRLPEGVSVRTFVPGQDDAAWLA VNA AAFAHPE  
QGSLTQRDLDDRKAEPWFDPAGFFLAERDGELIGFHWTKVHAEERLGE  
VYVLGIRPDTQGGGLGKALTTIGLRHLEGQGLPTAMLYVDADNKAAVA  
VYERLGFVTHETDLMYRTET (SEQ ID NO: 17)

**Figure 10D**

MshD amino acid sequence of *Corynebacterium diphtheriae* (PMshDCd-Tr)

MIETSLASAS AALRDRVDEI LAAATREDGC APLSESFLNG  
LRRADDGHVH SCVMDSHDQV VGVAARDGDS AEVVVDPAFR  
RQGYGSFLIR HVVSQGVKNV WAHGDGAGAK AVAKALQLEQ  
TRQLLVMAVE GDRLVESAQL QVPSGFRVLA LNEAYESIPD  
IEQQWLRVNN EAFEWHPEQG GWDSARLAQA RDTQWFRESD  
VLFLIDTAKR TVAGFHWTKR HGDLAEGADG EVYVVVGLGSA  
YRRRGLGDLL IRMGLHHLEY EHARRVILYV EGDNESARRA  
YDALGFHVVE SHVTYSPQSS S (SEQ ID NO: 18)

**Figure 10E**

Nucleic acid sequence *mshD* *M. smegmatis*, including stop codon

GTGACCTCCACCGAGTGGCGCACCGGGCTCACGGGTGCCAGCAGG  
CAGAGATTGCGCGCTGATCGACGCGGCCACCACGCACGACGGTGT  
CGCGCCGGTCGGTACCAAGTGCTGCGGGAACTGGGACGCGACCGC  
ACCCGGCACCTGCTGACCAACCGACGACGACCGCGTGGTGGATACCT  
CAACCTCGCGCCTGCCGAGGGGGACGATCCGGCGATGGCCGAACTC  
GTCGTGCATCCGCAGGCCCAGCGCGGTATCGGTGCGGCCATGGC  
GCGCACCGCGCTGGCAGAGGGCGGGCGGGCGCCCGTATCTGGGCG  
CACGGCAACATCGCCGCCGCCAGGCGATGGCGTCATCGCTTCGCCT  
GGTGGTGGTGCCTGAGCTGCTGCAGATGCGCCGCCCTGACCGATC  
TGCCGCCGGTGCCTGACACCCCCGGCGTGCATCGCACCTACGCC  
GGCCCCGGCGACGACGCCAGAGATCCTGCGGGTCAACAAACGCCCGT  
TCTCGTGGCACCCGAGCAGGGCGTGA (SEQ ID NO: 48)

**Figure 10F**

MshA-Msmeg 1-----VRLATDLETPRRVAVLSVHTSPLAQPGTGDA  
 MshA-Mtub 1MAGVRHDDGSGLIAQRRPVRGEGATRSRGPSGPSNRNVSAADDPRRVALLAVHTSPLAQPGTGDA  
 SpsA-Anab 1-----MFQNKKHRIALISVSGDPAVEIGQEEA  
 PimB-Mtub 1-----VCGVRVAIVAESFLPQVN-----  
 \*-BOX I---|  
 MshA-Msmeg 32GGMNVYVLQTAQLARRGVEVEVFRATSSADAPVVPPVAGPFEGLDKNDLPTQLC  
 MshA-Mtub 66GGMNVYMLQSAHLARRGIEVEIFTRATASADPPVVRVAPGVLRNVVAGPFEGLDKYDLPTQLC  
 SpsA-Anab 28GGQNYYREVGYALAEQGWQVDMFTTRRISPDQAEIVQHSPNCRTIRLQAGPVEFIGRDHVFDYLP  
 PimB-Mtub 19-GVSNSVVKVLEHLRRTGHEALVIAPDTPPGEDRAERLHDGVRVHRVPSRMFPKVT--TLP LGVP  
 MshA-Msmeg 97AFTAGVLRAEATHEPGY-YDVVHSHY-WLSGQVGWLARDRWA VPLVHTAHTLAAVKNAALAAGDA  
 MshA-Mtub 131AFAAGVLRAEAVHEPGY-YDITVHSHY-WLSGQVGWLARDRWA VPLVHTAHTLAAVKNAALAAGDG  
 SpsA-Anab 93EFVAEFORFQK--RQGYNQQLIHTNY-WLSSWVGMO LKKOQPLVLVHTYHSLGAIKYQTIA-DI  
 PimB-Mtub 81TFR--MLRALR---GFDPDVVHLAS PALLGYGGLHAARRLGVPVAVYQTDVPGFASSYG--I  
 G242↓ D244  
 MshA-Msmeg 160PEPPLR A VGEQQVVDEADRLIVNTEV EAQOLVSLHNADRSRIDVVH PGV DLDVFTPGSRDAA RAV  
 MshA-Mtub 194PEPPLR T VGEQQVVDEADRLIVN T DEARQV ISLHGADPARIDVVH PGV DLDVFRPGDRRAARAA  
 SpsA-Anab 153PAIANQRLAIEKACLESVDTVVATSPQEQQHMRALVSKGRIEMI PCGT D INNFGNIEKSAAREK  
 PimB-Mtub 137PMTARA AAWFRHLHRLADRTLAPSTATMESLIAQGIP--RVHRWARGVDVQRFAPSARNEV LRR  
 R273↓ K278  
 MshA-Msmeg 225EGLPTDQKIVAFVGRIQPLKAPDILLRAAK-----LPGVRVLIAGG--PSGSGLAQPD TLVRLA  
 MshA-Mtub 259LGLPVDERVVAFVGRIQPLKAPDIVLRAAK-----LPGVRVII VAGG--PSGSGL ASPD GLVRLA  
 SpsA-Anab 218LGIEPDAK M VFYVGRFDPRKG IETL VRAVAQSRLRGEANLQLVIGGGSRPGQSDGRERDRIANIV  
 PimB-Mtub 200RWSFDGKPIVGFVGRILAPEKHV DRLTGLAAS-----GAVRLVIVG-----DGIDRAR  
 E354↓-----BOX II-----|  
 MshA-Msmeg 283DELGISDRVTFLPPQSREQLVN VYRAADLVAVPSYSES FGLVAVEAQA CGTPV VAAAVGGLPVAV  
 MshA-Mtub 317DELGISARVTFLPPQSHTDLATLFR AADLVAVPSYSES FGLVAVEAQA CGTPV VAAAVGGLPVAV  
 SpsA-Anab 283AELELNDCTTFAGRLDHEILPYY YAAADVCVVP SHYEPFGLV AIEAMASKTPVIA SNVGGLOFTV  
 PimB-Mtub 247LQSAMPT-AVFTGARYGKE LAEAYASMDV FVHSGEHETECQVVOE ALASGLPVIAPDAGGPRDLI  
 MshA-Msmeg 348ADGVSGALVD-GHDIGDWADT TISEVLDREPA-----ALSRASAEHAAQSWAHTV DALLAS YSRAM  
 MshA-Mtub 382RDGTTGTLVS-GHEVGQWADAI DHLRLCAGPRGRVMSRAAARHAATFSWENTT DALLAS YRRAI  
 SpsA-Anab 348VPEVTGLLAP-PODES AFA TAI DRLANPTWR-DQLGTAARQRVETTFSWAGVASQLSQLYTHLL  
 PimB-Mtub 311TPHRTGLLLPVGEFEHRLPDAVAHLVHERQR-----YALAAARRSVLGRSWPVVCDELLGHYEAVR  
 MshA-Msmeg 408SDYRARHPRPA-----ARRSGRRFSMRRGVRT  
 MshA-Mtub 446GEYNAERQR RRGGEVISDLVAVGKPRHWT PRRGVGA  
 SpsA-Anab 411TQNAPEKKEKE-----AVAA-----  
 PimB-Mtub 371GRRTTQAA-----

Figure 11

**MshA amino acid sequence of *M. smegmatis* (PMshAMs-Tr)**

VRLATDLETP RRVAVLSVHT SPLAQPGTGD AGGMNVYVLQ  
TALQLARRGV EVEVFTRATS SADAPVVPVA PGVLVRNVVA  
GPFEGLDKND LPTQLCAFTA GVLRAEATHE PGYYDVVHSH  
YWLSGQVGWL ARDRWA VPLV HTAHTLAAVK NAALAAGDAP  
EPPLRAVGEQ QVVDEADRLI VNTEVEAQQL VSLHNADRSR  
IDVVHPGVDL DVFTPGSRDA ARAVGLPTD QKIVAFVGRI  
QPLKAPDILL RAAAKLPGVR VLIAGGPSGS GLAQPDTLVR  
LADELGISDR VTFLPPQSRE QLVNVYRAAD LVAVPSYSES  
FGLVAVEAQQA CGTPVVAAAV GGLPVAVADG VSGALVDGHD  
IGDWADTISE VLDREPAALS RASAEHAAQF SWAHTVDALL  
ASYSRAMSDY RARHPRPAAR RSGRRFSMRR GVRT (SEQ ID NO: 19)

**Figure 12A**

MshA amino acid sequence of *M. tuberculosis* (PMshAMtG1002)

MAGVRHDDGS GLIAQRRPVR GEGATRSRG P SGPSNRNVSA  
ADDPRRVALL AVHTSPLAQ P GTGDAGGMNV YMLQSALHLA  
RRGIEVEIFT RATASADPPV VRVAPGV LVR NVVAGPFEGL  
DKYDLPTQLC AFAAGVLRAE AVHEPGYYDI VHSHYWLSGQ  
VGWLARDRWA VPLVHTAHTL AAVKNAALAD GDGPEPPLRT  
VGEQQVVDEA DRLIVNTDDE ARQVISLHGA DPARIDVVHP  
GVLDLVFRPG DRRAARAALG LPVDERVVAF VGRIQPLKAP  
DIVLRAAAKL PGVRIIVAGG PSGSGLASPD GLVRLADELG  
ISARVTFLPP QSHTDLATLF RAADLVAVPS YSESFGLVAV  
EAQACGTPVV AAAVGGLPVA VRDGITGTLV SGHEVGQWAD  
AIDHLLRLCA GPRGRVMSRA AARHAATFSW ENTTDALLAS  
YRRAIGEYNA ERQRRGGEVI SDLVAVGKPR HWTPRRGVGA (SEQ ID  
NO: 20)

**Figure 12B**

Nucleic acid sequence *mshA* *M. smegmatis*, including stop codon

GTGCGTCTAGCGACAGACCT  
CGAGACCCCCCGCCGCGTGGCGGTGTTGTCGGTACACACACCTCTCCGC  
TGGCGCAGCCGGGACCGGCGACGCGGGCGCATGAACGTCTACGT  
GTTGCAGACCGCGCTGCAACTGGCCC GGCGTGGCGTCGAGGTCGAG  
GTCTTCACCAGGGCCACGTCGTCGGCCGATGCGCCGGTCGTGCCTGT  
GGCGCCCGGTGTGCTGGTGCACACGTCGTGGCCGGCCGTTCGAAG  
GCCTCGACAAGAACGATCTGCCAACGCAGCTGTGCGCGTTACCGCG  
GGTGTGCTGCGCGCCGAGGGCGACCCACGAGGCCGGCTACTACGACG  
TCGTGCATTGCACTACTGGCTGTCCGGCCAGGTGGTGGCTGGCG  
CGCGACCGCTGGGCCGTGCCGCTGGTGCACACCGCGCACACGCTGG  
CCGCGGTCAAGAACGCCGACTCGCCGCGACGCACCCGAGCC  
GCCGCTGCGCGCGGTGGCGAACAAACAGGTGGTCGACGAGGCCGAC  
CGCCTCATCGTAACACCGAACGTCGAAGCGCAGCAACTGGTCTCGTT  
GCACAATGCCGACCGCTACGCATCGACGTCGTGCACCCGGCGTCG  
ATCTCGACGTGTTCACCCCCGGTTCGCGCACGCGGGCGCGCGTG  
TTCGGGCTTCCCACCGACCGAGAACGATCGTGGCGTTCGTGGCCGCAT  
CCAGCCGCTCAAGGCCCGACATCCTGCTGCGTGCCTGGCGCGAAAC  
TGCCCGCGTGCCTGCTGATCGCCGGTGGACCCCTCCGGATCGGGA  
CTTGCCCAACCGGACACGCTGGTTCGGCTCGCCGACGAACACTGGGTAT  
CAGTGACCGGGTGACGTTCTCCGCCGAGAGCCGAAACAACG  
GTCAACGTGTACCGGGCGGCCGATCTGGTCGCGGTGCCGAGCTACTC  
CGAGTCGTTGGCCTGGTCGCCGTCGAGGCACGGCGTGCACGC  
CCGTCGTCGCCGCCGCGTGGCGGACTGCCGGTGCACGGCGAC  
GGCGTCAGCGGGGCACTCGTCGACGGCCACGACATCGCGACTGGG  
CCGACACCATCAGCGAGGTGCTCGACCGCAGGCCGCCGCTGAG  
CCGCGCCTCCGCCGAAACACGCCGCTCAGTTCTCGTGGCGCACACCG  
TCGACGCGCTGCTGCCAGCTACAGCCGGCCAT  
GAGTGACTACCGGGCCGTCATCCCAGACCCGCCGCGCGGCGTTCCG  
GACGCCGGTTCTCGATGCGCAGGGAGTACGCACGTGA (SEQ ID NO:  
49)

**Figure 12C**

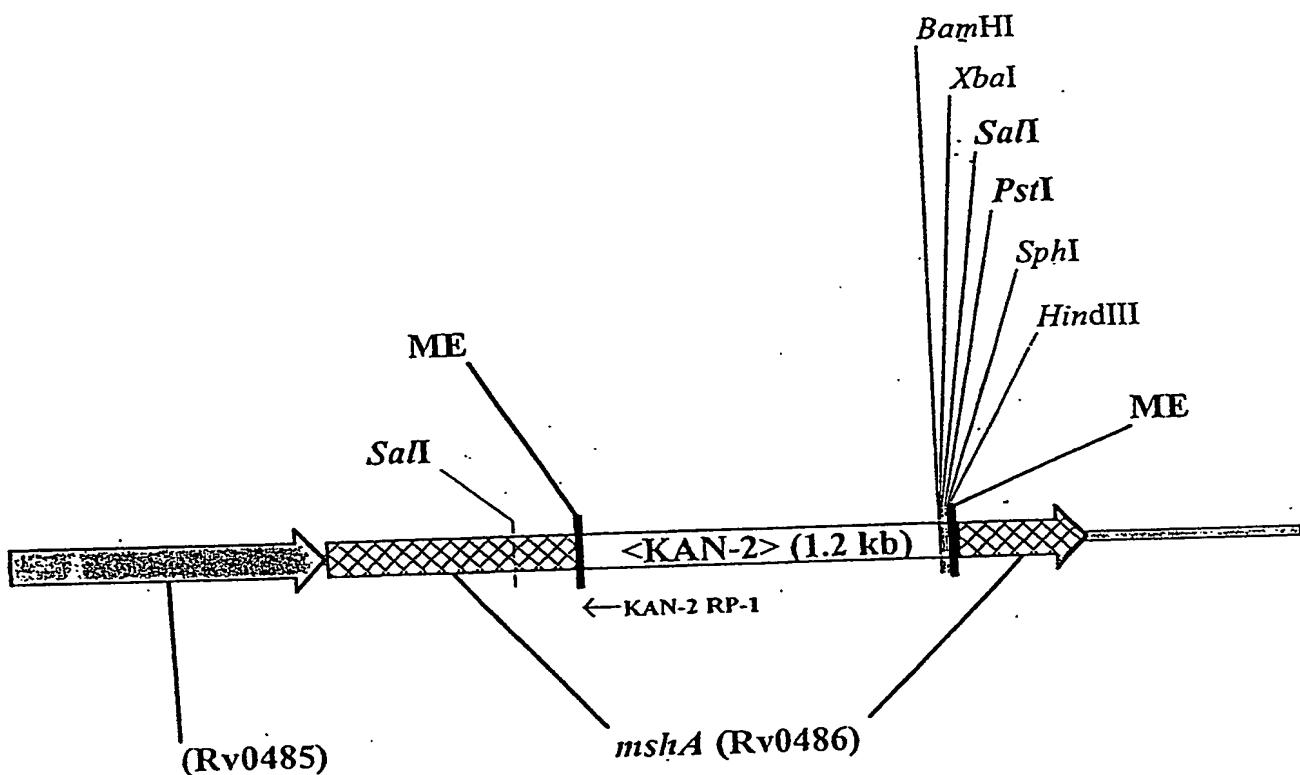
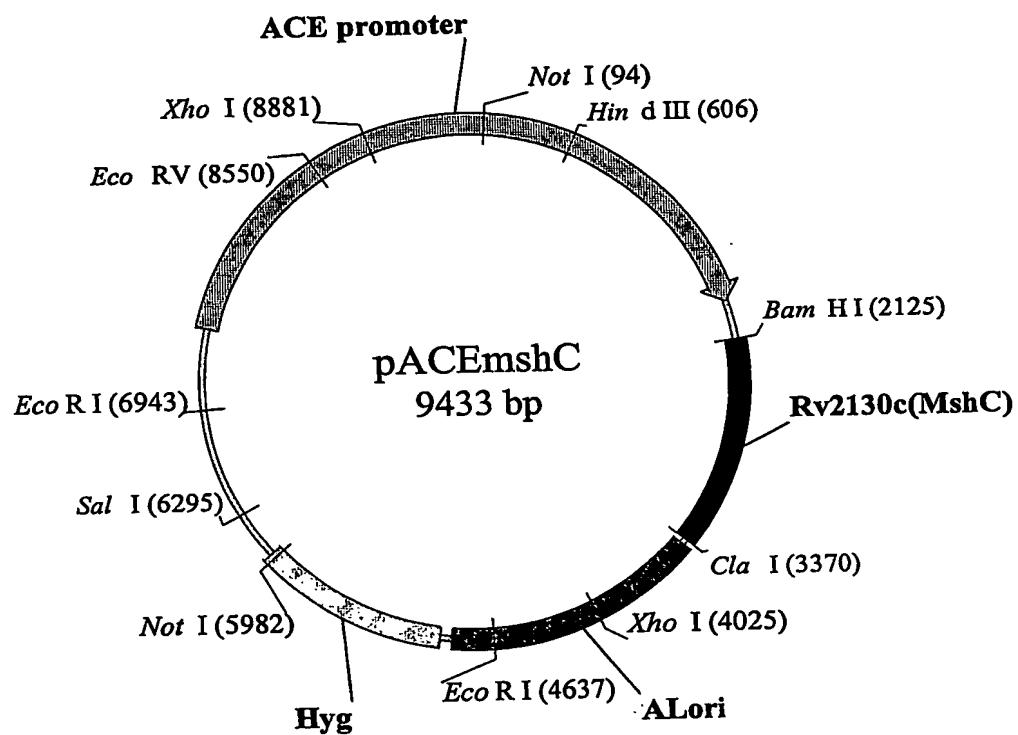
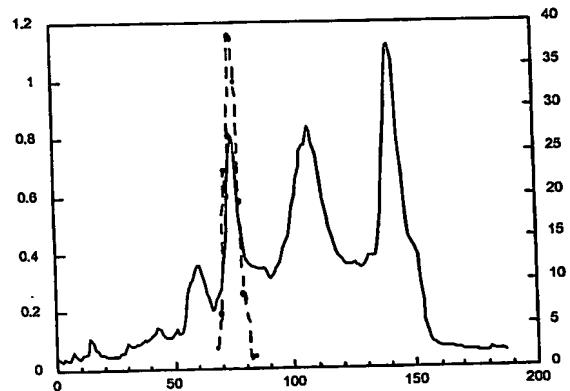
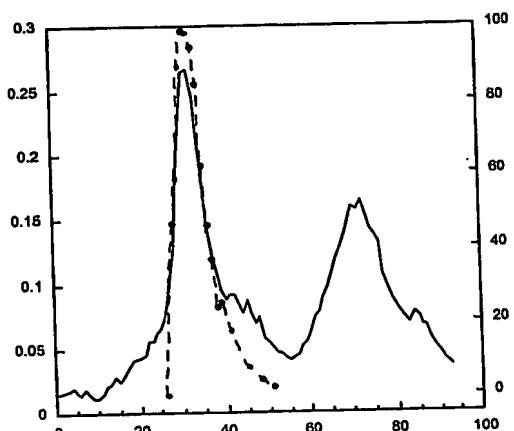


Figure 13

**Figure 14**



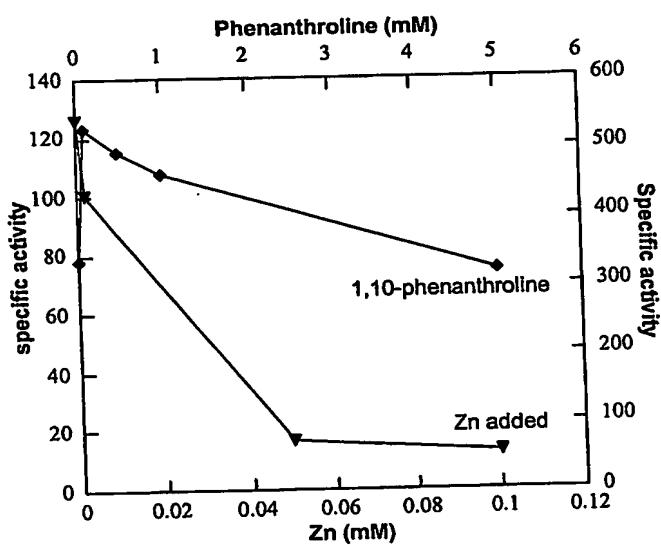
(A) DEAE-M profile



(B) Hydroxyapatite profile

**Figure 15**

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**Figure 16**

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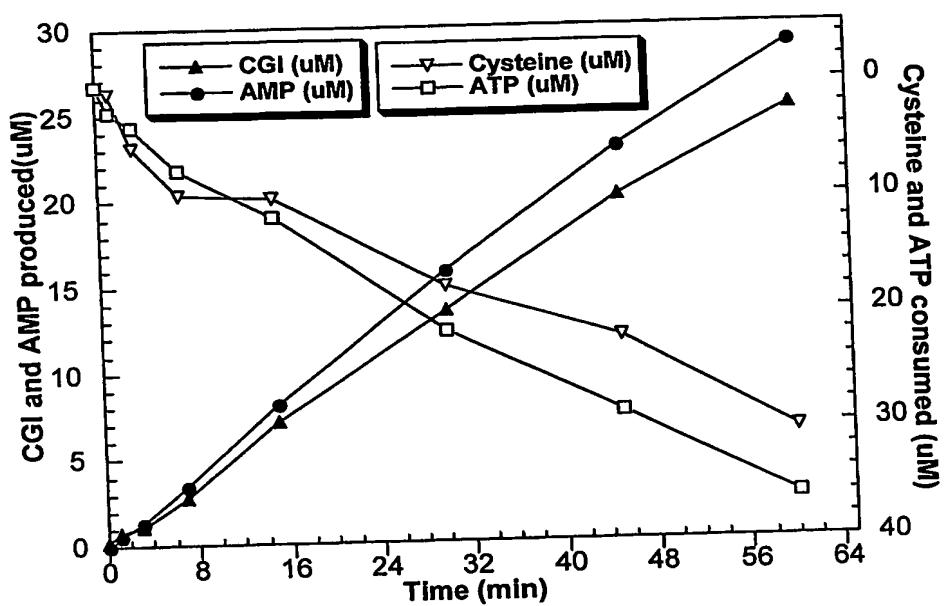


Figure 17

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## (a) First Half of Rossman fold:

*M. smeg* MshC (40) --MYVCGITPYDATHLGHAAATYLTFDL (64)  
*M. lepr* MshC (11) ATMYVCGITPYDATHLGHAAATYLAFDL (37)  
*S. coel.* MshC (40) --IYVCGITPYDATHMGHAAATYNAFDL (64)  
*C. strt.* MshC (44) --MYVCGITPYDSTLGHAAATYLTFDL (68)  
*T. bifd.* MshC (40) --MYVCGITPYDAAHLGHAFTYLTFDL (64)  
*M. tubr* CySS (30) --IYLCGATVQGLPHIGHVRSGVAFDI (54)  
*E. coli* CySS (25) --MYVCGITVYDLCHIGHGRTFVAFDV (49)

## (b) Second half of Rossman Fold:

*M. smeg* MshC (218) SPFGRGRGPWHEVCSAIALTRIGTGLDI QGGGSDLI FPHHEYSAAHAEESVT  
*M. lepr* MshC (190) SPFGPGRGPWHEVCAAILSRIGIGLDI QGGGSDLI FPHHEFTAAHAECVR  
*S. coel.* MshC (215) GTLGRGRGPWHEVIECVAI ALDHGMGFDV QGGGSDLI FPHHEFTAAHAQALT  
*C. strt.* MshC (219) SPFGPGRGPWHEVCSAIALNRIGSHEAI QGGGSDLI FPHHEFTAAHAEEAAL  
*T. bifd.* MshC (198) TPLGRGRGPWHEVCSAISVHELGMGFDLNGGGDDL I FPHHEMGAEEACCAT  
*M. tubr* CySS (214) TPWGRGRGPWHELECSAMARSYILGPEFDI HCGMDLIVEPPHHENELAQSRAG  
*E. coli* CySS (196) SPWGAGRGPHEVIECSAMNCQLGNHEDI HGGGSDLI FPHHEQSTCAH

*M. smeg* MshC GERRFARHYVBGMIGWDGHKMSKS (293)  
*M. lepr* MshC GERRFARHYVHAGMIIGWDEHKMSKS (265)  
*S. coel.* MshC GEFPMAKAYVHAGMIAGLDGERMSKS (290)  
*C. strt.* MshC KVERMAGHYVHAGMIALDGKVMSKS (294)  
*T. bifd.* MshC GSRPQARHYLHVAMVGLDGKEMSKS (289)  
*M. tubr* CySS DG--FARYWLHNGWVTMGGERMSKS (271)  
*E. coli* CySS DGQ-YVNYYWMHSGMVMDREKMSKS (270)

Figure 18

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